

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANT: Li, ET AL.
- (ii) TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGMR10
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN
- (B) STREET: 6 BECKER FARM ROAD
- (C) CITY: ROSELAND
- (D) STATE: NEW JERSEY
- (E) COUNTRY: USA
- (F) ZIP: 07068
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5 INCH DISKETTE
- (B) COMPUTER: IBM PS/2
- (C) OPERATING SYSTEM: MS-DOS
- (D) SOFTWARE: WORD PERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/466,343
- (B) FILING DATE: June 6, 1995
- (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: FERRARO, GREGORY D.
- (B) REGISTRATION NUMBER: 36,184
- (C) REFERENCE/DOCKET NUMBER: 325800-449
- (viii) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 201-994-1700
- (B) TELEFAX: 201-994-1744
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 1414 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGAGATGGT GCTTTCATGA ATTCCCCCAA CAAGAGCCAA GCTCTCCATC TAGTGGACAG 60

GGAAGGTAGC AGCAAACCTT CCCTTCACTA CGAAACTTCA TTGCTTGGCC CAAAAGAGAG 120
 TTAATTCAAT GTAGACATCT ATGTAGGCAA TTAAAAACCT ATTGATGTAT AAAACAGTTT 180
 GCATTCATGG AGGGCAACTA AATACATTCT AGGACTTTAT AAAAGATCAC TTTTATTATTA 240
 TGCACAGGGT GGAACAAG ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC 291
 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp
 ATC AAT TAT TAT ACA TCG GAG CCC TGC CCA AAA ATC AAT GTG AAG CAA 339
 Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln
 ATC GCA GCC CGC CTC CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT 387
 Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe
 GGT TTT GTG GGC AAC ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC CAA 435
 Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln
 AGG CTG GAG AGC ATG ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT 483
 Arg Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser
 GAC CTG TTT TTC CTT CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC 531
 Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala
 GCC CAG TGG GAC TTT GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC 579
 Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Leu Leu Thr Gly Leu Tyr
 TAT TTT ATA GGC TTC TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA 627
 Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Gln Leu Leu Thr
 ATC GAT AGG TAC CTG GCT ATC GTC CAT GCT GTG TTT GCT TTA AAA GCC 675
 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala
 AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG 723
 Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Val Val
 GCT GTG TTT GCG TCT CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA 771
 Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys
 GAA GGT CTT CAT TAC ACC TGC AGC TCT CAT TTT CCA TAC AGT CAG TAT 819
 Glu Gly Leu His Tyr Thr cys Ser Ser His Phe Pro Tyr Ser Gln Tyr
 CAA TTC TGG AAG AAT TTC CAG ACA TTA AAG ATA GTC ATC TTG GGG CTG 867
 Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu
 GTC CTG CCG CTG CTT GTC ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA 915
 Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys
 ACT CTG CTT CGG TGT CGA AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG 963
 Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg
 CTT ATC TTC ACC ATC ATG ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC 1011
 Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr
 AAC ATT GTC CTT CTC CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT 1059
 Asn Ile Val Leu Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn
 AAT TGC AGT AGC TCT AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG 1107
 Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu
 ACT CTT GGG ATG ACG CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT 1155
 Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe

GTC GGG GAG AAG TTC AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC 1203
 Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His
 ATT GCC AAA CGC TTC TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT 1251
 Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala
 CCC GAG CGA GCA AGC TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA 1299
 Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu
 ATA TCT GTG GGC TTG TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG 1354
 Ile Ser Val Gly Leu
 TGCACATGGC TTAGTTTCA TACACAGCCT GGGCTGGGGG TGGGGTGGAA GAGGTCTTTT 1414

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: AMINO ACIDS

(B) TYPE: AMINO ACID

(C) STRANDEDNESS:

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr
 5 10 15
 Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln Ile Ala Ala
 20 25 30
 Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe
 35 40 45
 Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln Arg
 50 55 60
 Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser
 65 70 75
 Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala
 80 85 90
 Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Leu Leu Thr Gly
 95 100 105
 Leu Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Gln
 110 115 120
 Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
 125 130 135
 Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val
 140 145 150
 Ile Thr Trp Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile
 155 160 165
 Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr Thr cys Ser Ser
 170 175 180
 His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr
 185 190 195
 Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu Val Met
 200 205 210

Val	Ile	Cys	Tyr	Ser	Gly	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Cys	Arg	
				215					220					225	
Asn	Glu	Lys	Lys	Arg	His	Arg	Ala	Val	Arg	Leu	Ile	Phe	Thr	Ile	
				230					235					240	
Met	Ile	Val	Tyr	Phe	Leu	Phe	Trp	Ala	Pro	Tyr	Asn	Ile	Val	Leu	
				245					250					255	
Leu	Leu	Asn	Thr	Phe	Gln	Glu	Phe	Phe	Gly	Leu	Asn	Asn	Cys	Ser	
				260					265					270	
Ser	Ser	Asn	Arg	Leu	Asp	Gln	Ala	Met	Gln	Val	Thr	Glu	Thr	Leu	
				275					280					285	
Gly	Met	Thr	His	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Val	
				290					295					300	
Gly	Glu	Lys	Phe	Arg	Asn	Tyr	Leu	Leu	Val	Phe	Phe	Gln	Lys	His	
				305					310					315	
Ile	Ala	Lys	Arg	Phe	Cys	Lys	Cys	Cys	Ser	Ile	Phe	Gln	Gln	Glu	
				320					325					330	
Ala	Pro	Glu	Arg	Ala	Ser	Ser	Val	Tyr	Thr	Arg	Ser	Thr	Gly	Glu	
				335					340					345	
Gln	Glu	Ile	Ser	Val	Gly	Leu									
				350											

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 30 BASE PAIRS
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGAATTCCT CCATGGATTA TCAAGTGTCA

30

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 29 BASE PAIRS
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGAAGCTTC GTCACAAGCC CACAGATAT

29

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 34 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCAAGCTT GCCACCATGG ATTATCAAGT GTCA

34

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 61 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CCGATGGGTA GCACAAGCCC ACAGATATTT 60
C 61

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 30 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGGATCCCT CCATGGATTA TCAAGTGTCA

30

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 29 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGGATCCCG CTCACAAGCC CACAGATAT

29